



1600

RAW SEQUENCE LISTING

DATE: 11/07/2003

PATENT APPLICATION: US/09/826,115A

TIME: 14:27:33

Input Set : A:\64908 seq.txt

Output Set: N:\CRF4\11062003\I826115A.raw

3 <110> APPLICANT: The Government of the United States of America, as
 4 represented by the Secretary, Department of Health and Human
 5 Services, c/o Centers for Disease Control and Prevention
 6 Chang, Gwong-Jen J.
 8 <120> TITLE OF INVENTION: NUCLEIC ACID VACCINES FOR PREVENTION OF FLAVIVIRUS INFECTION
 10 <130> FILE REFERENCE: 6395-64908
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/826,115A
 C--> 12 <141> CURRENT FILING DATE: 2001-04-04
 12 <150> PRIOR APPLICATION NUMBER: PCT/US02/10764
 13 <151> PRIOR FILING DATE: 2002-04-04
 15 <150> PRIOR APPLICATION NUMBER: 09/826,115
 16 <151> PRIOR FILING DATE: 2001-04-04
 18 <150> PRIOR APPLICATION NUMBER: 09/701,536
 19 <151> PRIOR FILING DATE: 2000-11-29
 21 <150> PRIOR APPLICATION NUMBER: PCT/US99/12298
 22 <151> PRIOR FILING DATE: 1999-06-03
 24 <150> PRIOR APPLICATION NUMBER: 60/087,908
 25 <151> PRIOR FILING DATE: 1998-06-04
 27 <160> NUMBER OF SEQ ID NOS: 61
 29 <170> SOFTWARE: PatentIn version 3.2
 31 <210> SEQ ID NO: 1
 32 <211> LENGTH: 48
 33 <212> TYPE: DNA
 34 <213> ORGANISM: Artificial Sequence
 36 <220> FEATURE:
 37 <223> OTHER INFORMATION: Description of artificial sequence; note = synthetic
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 40 <220> FEATURE:
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 42 <222> LOCATION: (1)..(48)
 43 <223> OTHER INFORMATION: Amplimer 14DV389
 45 <220> FEATURE:
 46 <221> NAME/KEY: CDS
 47 <222> LOCATION: (25)..(48)
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 51 Met Gly Arg Lys Gln Asn Lys Arg
 52 1 5
 55 <210> SEQ ID NO: 2
 56 <211> LENGTH: 8
 57 <212> TYPE: PRT
 58 <213> ORGANISM: Artificial Sequence
 60 <220> FEATURE:
 61 <223> OTHER INFORMATION: Description of artificial sequence; note = synthetic

ENTERED

construct

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80 <222> LOCATION: (1)..(50)
81 <223> OTHER INFORMATION: Amplimer c14DV2453
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98 <222> LOCATION: (1)..(48)
99 <223> OTHER INFORMATION: Amplimer YFDV389
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103 <222> LOCATION: (25)..(48)
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107 Met Arg Ser His Asp Val Leu Thr
108 1 5
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136 <222> LOCATION: (1)..(41)
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145 <212> TYPE: DNA
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154 <222> LOCATION: (1)..(51)
155 <223> OTHER INFORMATION: Amplimer SLEDV410
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159 <222> LOCATION: (25)..(51)
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193 <223> OTHER INFORMATION: Amplimer cSLEDV2449
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204 <220> FEATURE:
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211 <223> OTHER INFORMATION: pCDJE 2-7
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217 <400> SEQUENCE: 10
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220 ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg      120
222 cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc      180
224 ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt      240
226 gattattgac tagttattaa tagtaatcaa ttacgggggtc attagttcat agcccatata      300
228 tggagtcccg cgttacataa cttacggtaa atggcccggc tggctgaccg cccaacgacc      360
230 cccgccatt gacgtcaata atgacgtatg tccccatagt aacgccataa gggactttcc      420
232 attgacgtca atgggtggac tatttacggg aaactgccc cttggcagta catcaagtgt      480
234 atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt      540
236 atgccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca      600
238 tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg      660
240 actcacggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc      720
242 aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg      780
244 gtaggcgtgt acgggtgggag gtctatataa gcagagctct ctggctaact agagaaccca      840
246 ctgcttactg gcttatcgaa attaatacga ctactatag ggagacccaa gcttgggtacc      900
248 gagctcgccg ccgcc atg ggc aga aag caa aac aaa aga gga gga aat gaa      951
249           Met Gly Arg Lys  Gln Asn Lys Arg Gly Gly Asn Glu
250           1             5             10
252 ggc tca atc atg tgg ctc gcg agc ttg gca gtt gtc ata gct tgt gcg      999
253 Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala
254           15             20             25
256 gga gcc atg aag ttg tcg aat ttc cag ggg aag ctt ttg atg acc atc      1047
257 Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile
258           30             35             40
260 aac aac acg gac att gca gac gtt atc gtg att ccc acc tca aaa gga      1095
261 Asn Asn Thr Asp Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly
262 45             50             55             60
264 gag aac aga tgc tgg gtc cgg gca atc gac gtc ggc tac atg tgt gag      1143
265 Glu Asn Arg Cys Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu
266           65             70             75
268 gac act atc acg tac gaa tgt cct aag ctt acc atg ggc aat gat cca      1191
269 Asp Thr Ile Thr Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro
270           80             85             90
272 gag gat gtg gat tgc tgg tgt gac aac caa gaa gtc tac gtc caa tat      1239
273 Glu Asp Val Asp Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr
274           95             100            105
276 gga cgg tgc acg cgg acc agg cat tcc aag cga agc agg aga tcc gtg      1287
277 Gly Arg Cys Thr Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val
278           110            115            120
280 tcg gtc caa aca cat ggg gag agt tca cta gtg aat aaa aaa gag gct      1335
281 Ser Val Gln Thr His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala
282 125            130            135            140

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285	Trp	Leu	Asp	Ser	Thr	Lys	Ala	Thr	Arg	Tyr	Leu	Met	Lys	Thr	Glu	Asn	
286					145					150					155		
288	tgg	atc	ata	agg	aat	cct	ggc	tat	gct	ttc	ctg	gcg	gcg	gta	ctt	ggc	1431
289	Trp	Ile	Ile	Arg	Asn	Pro	Gly	Tyr	Ala	Phe	Leu	Ala	Ala	Val	Leu	Gly	
290				160					165					170			
292	tgg	atg	ctt	ggc	agt	aac	aac	ggt	caa	cgc	gtg	gta	ttt	acc	atc	ctc	1479
293	Trp	Met	Leu	Gly	Ser	Asn	Asn	Gly	Gln	Arg	Val	Val	Phe	Thr	Ile	Leu	
294			175					180					185				
296	ctg	ctg	ttg	gtc	gct	ccg	gct	tac	agt	ttt	aat	tgt	ctg	gga	atg	ggc	1527
297	Leu	Leu	Leu	Val	Ala	Pro	Ala	Tyr	Ser	Phe	Asn	Cys	Leu	Gly	Met	Gly	
298		190					195					200					
300	aat	cgt	gac	ttc	ata	gaa	gga	gcc	agt	gga	gcc	act	tgg	gtg	gac	ttg	1575
301	Asn	Arg	Asp	Phe	Ile	Glu	Gly	Ala	Ser	Gly	Ala	Thr	Trp	Val	Asp	Leu	
302	205				210					215					220		
304	gtg	ctg	gaa	gga	gat	agc	tgc	ttg	aca	atc	atg	gca	aac	gac	aaa	cca	1623
305	Val	Leu	Glu	Gly	Asp	Ser	Cys	Leu	Thr	Ile	Met	Ala	Asn	Asp	Lys	Pro	
306				225					230					235			
308	aca	ttg	gac	gtc	cgc	atg	att	aac	atc	gaa	gct	agc	caa	ctt	gct	gag	1671
309	Thr	Leu	Asp	Val	Arg	Met	Ile	Asn	Ile	Glu	Ala	Ser	Gln	Leu	Ala	Glu	
310			240					245					250				
312	gtc	aga	agt	tac	tgc	tat	cat	gct	tca	gtc	act	gac	atc	tcg	acg	gtg	1719
313	Val	Arg	Ser	Tyr	Cys	Tyr	His	Ala	Ser	Val	Thr	Asp	Ile	Ser	Thr	Val	
314			255					260					265				
316	gct	cgg	tgc	ccc	acg	act	gga	gaa	gcc	cac	aac	gag	aag	cga	gct	gat	1767
317	Ala	Arg	Cys	Pro	Thr	Thr	Gly	Glu	Ala	His	Asn	Glu	Lys	Arg	Ala	Asp	
318		270					275					280					
320	agt	agc	tat	gtg	tgc	aaa	caa	ggc	ttc	act	gac	cgt	ggg	tgg	ggc	aac	1815
321	Ser	Ser	Tyr	Val	Cys	Lys	Gln	Gly	Phe	Thr	Asp	Arg	Gly	Trp	Gly	Asn	
322	285				290					295					300		
324	gga	tgt	gga	ctt	ttc	ggg	aag	gga	agc	att	gac	aca	tgt	gca	aaa	ttc	1863
325	Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly	Ser	Ile	Asp	Thr	Cys	Ala	Lys	Phe	
326				305					310				315				
328	tcc	tgc	acc	agt	aaa	gcg	att	ggg	aga	aca	atc	cag	cca	gaa	aac	atc	1911
329	Ser	Cys	Thr	Ser	Lys	Ala	Ile	Gly	Arg	Thr	Ile	Gln	Pro	Glu	Asn	Ile	
330			320					325					330				
332	aaa	tac	gaa	gtt	ggc	att	ttt	gtg	cat	gga	acc	acc	act	tcg	gaa	aac	1959
333	Lys	Tyr	Glu	Val	Gly	Ile	Phe	Val	His	Gly	Thr	Thr	Thr	Ser	Glu	Asn	
334			335					340					345				
336	cat	ggg	aat	tat	tca	gcg	caa	gtt	ggg	gcg	tcc	cag	gcg	gca	aag	ttt	2007
337	His	Gly	Asn	Tyr	Ser	Ala	Gln	Val	Gly	Ala	Ser	Gln	Ala	Ala	Lys	Phe	
338		350					355					360					
340	aca	gta	aca	ccc	aat	gct	cct	tcg	ata	acc	ctc	aaa	ctt	ggt	gac	tac	2055
341	Thr	Val	Thr	Pro	Asn	Ala	Pro	Ser	Ile	Thr	Leu	Lys	Leu	Gly	Asp	Tyr	
342	365				370					375					380		
344	gga	gaa	gtc	aca	ctg	gac	tgt	gag	cca	agg	agt	gga	ctg	aac	act	gaa	2103
345	Gly	Glu	Val	Thr	Leu	Asp	Cys	Glu	Pro	Arg	Ser	Gly	Leu	Asn	Thr	Glu	
346				385				390					395				
348	gcg	ttt	tac	gtc	atg	acc	gtg	ggg	tca	aag	tca	ttt	ctg	gtc	cat	agg	2151

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date